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TECH CENTER 1600/2900

1638



#13 1600

RAW SEQUENCE LISTING

DATE: 08/08/2002

PATENT APPLICATION: US/09/714,767A

TIME: 21:11:09

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\08082002\I714767A.raw

ENTERED

4 <110> APPLICANT: Bidney, Dennis
 5 Duvick, Jon
 6 Hendrick, Carol
 7 Hu, Xu
 8 Lu, Guihua
 9 Crasta, Oswald
 12 <120> TITLE OF INVENTION: Sunflower RhoGAP, LOX, ADH and SCIP -
 13 Polynucleotides and Methods of Use
 16 <130> FILE REFERENCE: 35718/201902
 18 <140> CURRENT APPLICATION NUMBER: 09/714,767A
 19 <141> CURRENT FILING DATE: 2000-11-16
 21 <150> PRIOR APPLICATION NUMBER: US 60/166,128
 22 <151> PRIOR FILING DATE: 1999-11-18
 24 <150> PRIOR APPLICATION NUMBER: US 60/201,837
 25 <151> PRIOR FILING DATE: 2000-05-03
 27 <160> NUMBER OF SEQ ID NOS: 10
 29 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 31 <210> SEQ ID NO: 1
 32 <211> LENGTH: 824
 33 <212> TYPE: DNA
 34 <213> ORGANISM: Helianthus annuus
 36 <220> FEATURE:
 37 <221> NAME/KEY: misc_feature
 38 <222> LOCATION: (0)...(0)
 39 <223> OTHER INFORMATION: rhoGAP
 41 <221> NAME/KEY: CDS
 42 <222> LOCATION: (35)...(637)

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W--> 44 <400> 1

45	ttcggcacga gtccaaatcc aatcttcaat cacc atg gct gaa gaa caa ctg ccg	55
46	Met Ala Glu Glu Gln Leu Pro	
47	1 5	
49	cct gat caa att aaa ctc att cac aag ctt aat ttg ttc aaa atc aaa	103
50	Pro Asp Gln Ile Lys Leu Ile His Lys Leu Asn Leu Phe Lys Ile Lys	
51	10 15 20	
53	ggc aga gat aaa cac aat cgc aaa atc tta cga att gtc gga aaa aac	151
54	Gly Arg Asp Lys His Asn Arg Lys Ile Leu Arg Ile Val Gly Lys Asn	
55	25 30 35	
57	ttt cca gct aag agt ttg acc gtt gac ctg ttg aaa aaa tat cta gaa	199
58	Phe Pro Ala Lys Ser Leu Thr Val Asp Leu Lys Lys Tyr Leu Glu	
59	40 45 50 55	
61	gtg aaa att ttc ccc aaa ctt gaa cga ccg ttt gtg gtg gtt tac gtt	247
62	Val Lys Ile Phe Pro Lys Leu Glu Arg Pro Phe Val Val Val Tyr Val	
63	60 65 70	

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65 cac act gat gtt cag aag agc gag aat ttc cct gga ata tcc gtt ctc      295
66 His Thr Asp Val Gln Lys Ser Glu Asn Phe Pro Gly Ile Ser Val Leu
67          75          80          85
69 cgg tca gtt tac gac gcg att ccg atg acc gtg aaa caa tat ctt gag      343
70 Arg Ser Val Tyr Asp Ala Ile Pro Met Thr Val Lys Gln Tyr Leu Glu
71          90          95          100
73 gcg gtt tac ttt gtt cat ccg gat ctg cag tcc aga att ttt ctg gct      391
74 Ala Val Tyr Phe Val His Pro Asp Leu Gln Ser Arg Ile Phe Leu Ala
75      105          110          115
77 aca ttt ggc cgg ctt atc ttc acc gga ggg tta tat gca aag ctg aga      439
78 Thr Phe Gly Arg Leu Ile Phe Thr Gly Gly Leu Tyr Ala Lys Leu Arg
79 120          125          130          135
81 ttt gtg agt cga ttg gcg tat ctg tgg gaa cat gtg aaa agg aac gag      487
82 Phe Val Ser Arg Leu Ala Tyr Leu Trp Glu His Val Lys Arg Asn Glu
83          140          145          150
85 atc gag atc cca gag ttt gtc tac gat cat gat gag gat ctg gag tac      535
86 Ile Glu Ile Pro Glu Phe Val Tyr Asp His Asp Glu Asp Leu Glu Tyr
87          155          160          165
89 cgt ccg atg atg gat tac ggg ata gag agt gac cac gct aga gtt tat      583
90 Arg Pro Met Met Asp Tyr Gly Ile Glu Ser Asp His Ala Arg Val Tyr
91      170          175          180
93 gga gcg ccc gcg gtt gat tcc tct gtg gcg gct tat tcc atg agg tgt      631
94 Gly Ala Pro Ala Val Asp Ser Ser Val Ala Ala Tyr Ser Met Arg Cys
95      185          190          195
97 atc tca taggggaaat agttgttttt tcttttgttt ttgaaaatag gtgctaaaag      687
98 Ile Ser
99 200
101 aagtgcataa tatagtattt agcaatattt cgggtgttgt agtatgttga taacgggctt      747
102 ttcttataac attcattgtt ctagttttct tttgtaaaaa ttatttgata aattctttgt      807
103 aaaaaaaaaa aaaaaaa
105 <210> SEQ ID NO: 2
106 <211> LENGTH: 201
107 <212> TYPE: PRT
108 <213> ORGANISM: Helianthus annuus
110 <400> SEQUENCE: 2
111 Met Ala Glu Glu Gln Leu Pro Pro Asp Gln Ile Lys Leu Ile His Lys
112 1          5          10          15
113 Leu Asn Leu Phe Lys Ile Lys Gly Arg Asp Lys His Asn Arg Lys Ile
114          20          25          30
115 Leu Arg Ile Val Gly Lys Asn Phe Pro Ala Lys Ser Leu Thr Val Asp
116      35          40          45
117 Leu Leu Lys Lys Tyr Leu Glu Val Lys Ile Phe Pro Lys Leu Glu Arg
118      50          55          60
119 Pro Phe Val Val Val Tyr Val His Thr Asp Val Gln Lys Ser Glu Asn
120 65          70          75          80
121 Phe Pro Gly Ile Ser Val Leu Arg Ser Val Tyr Asp Ala Ile Pro Met
122          85          90          95
123 Thr Val Lys Gln Tyr Leu Glu Ala Val Tyr Phe Val His Pro Asp Leu
124          100          105          110

```

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125 Gln Ser Arg Ile Phe Leu Ala Thr Phe Gly Arg Leu Ile Phe Thr Gly
 126 115 120 125
 127 Gly Leu Tyr Ala Lys Leu Arg Phe Val Ser Arg Leu Ala Tyr Leu Trp
 128 130 135 140
 129 Glu His Val Lys Arg Asn Glu Ile Glu Ile Pro Glu Phe Val Tyr Asp
 130 145 150 155 160
 131 His Asp Glu Asp Leu Glu Tyr Arg Pro Met Met Asp Tyr Gly Ile Glu
 132 165 170 175
 133 Ser Asp His Ala Arg Val Tyr Gly Ala Pro Ala Val Asp Ser Ser Val
 134 180 185 190
 135 Ala Ala Tyr Ser Met Arg Cys Ile Ser
 136 195 200

137 <210> SEQ ID NO: 3

138 <211> LENGTH: 2945

139 <212> TYPE: DNA

140 <213> ORGANISM: Helianthus annuus

142 <220> FEATURE:

143 <221> NAME/KEY: misc_feature

144 <222> LOCATION: (0)...(0)

145 <223> OTHER INFORMATION: lox cDNA

147 <221> NAME/KEY: CDS

148 <222> LOCATION: (19)...(2721)

W--> 150 <400> 3

151 cggcaccgaga agaaaacc atg ttg aat tct caa atc aac cat tct cac cct 51
 152 Met Leu Asn Ser Gln Ile Asn His Ser His Pro
 153 1 5 10
 155 ctt aac aac cta cta cca atc cgc aaa gcc ttt gtc cat ggt gac acc 99
 156 Leu Asn Asn Leu Leu Pro Ile Arg Lys Ala Phe Val His Gly Asp Thr
 157 15 20 25
 159 act aac cat tcc tcc tcc aac gcc tac tcc ccc gcc aac ctt cgc caa 147
 160 Thr Asn His Ser Ser Ser Asn Ala Tyr Ser Pro Ala Asn Leu Arg Gln
 161 30 35 40
 163 cac gcg tcc acc aag aaa tcc aat gct acc cgt gca cga tcc acc tca 195
 164 His Ala Ser Thr Lys Lys Ser Asn Ala Thr Arg Ala Arg Ser Thr Ser
 165 45 50 55
 167 act gcg ggt aac att aaa gcc ata tca atc ccc ttt ctt acc aag gag 243
 168 Thr Ala Gly Asn Ile Lys Ala Ile Ser Ile Pro Phe Leu Thr Lys Glu
 169 60 65 70 75
 171 acc acc gtc aag tgt gtc atc acc gtc caa cca acc att agt tcc gcc 291
 172 Thr Thr Val Lys Cys Val Ile Thr Val Gln Pro Thr Ile Ser Ser Ala
 173 80 85 90
 175 att gct ggt gta ggc gtt ggt ggt att gtt gat ggt gtt tct gat ctt 339
 176 Ile Ala Gly Val Gly Val Gly Gly Ile Val Asp Gly Val Ser Asp Leu
 177 95 100 105
 179 cta ggg ttg tca ttt ttg ttg gag ctg gtt tca aat gac ctg gat tca 387
 180 Leu Gly Leu Ser Phe Leu Leu Glu Leu Val Ser Asn Asp Leu Asp Ser
 181 110 115 120
 183 aaa gga aac caa aag aca gtg aag gct tat gca aga tac aac gca ctg 435
 184 Lys Gly Asn Gln Lys Thr Val Lys Ala Tyr Ala Arg Tyr Asn Ala Leu

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Input Set : A:\PTO.AMC.txt

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185	125	130	135	
187	gat ttg gac att agc gtg tac aca tac aaa tgc gac ttc gac gtc cct	483		
188	Asp Leu Asp Ile Ser Val Tyr Thr Tyr Lys Cys Asp Phe Asp Val Pro			
189	140 145 150 155			
191	gaa gat ttt ggg gag ata gga gct gtg ttg gta gaa aat gag tat agc	531		
192	Glu Asp Phe Gly Glu Ile Gly Ala Val Leu Val Glu Asn Glu Tyr Ser			
193	160 165 170			
195	aag aag atg ttt ttc aag aac att gtt ctt aac aac ggt gtt acc ttc	579		
196	Lys Lys Met Phe Phe Lys Asn Ile Val Leu Asn Asn Gly Val Thr Phe			
197	175 180 185			
199	aca tgc gag tca tgg gtt cac tcc aaa tac gat aac cct gag aaa aga	627		
200	Thr Cys Glu Ser Trp Val His Ser Lys Tyr Asp Asn Pro Glu Lys Arg			
201	190 195 200			
203	ata ttt ttc acc gac aag tcg tat cta ccg ttg gaa acg ccg acg gca	675		
204	Ile Phe Phe Thr Asp Lys Ser Tyr Leu Pro Leu Glu Thr Pro Thr Ala			
205	205 210 215			
207	ctg aag ccg tta cga gag aaa gat atg gaa tcg ctt cga gga aac ggc	723		
208	Leu Lys Pro Leu Arg Glu Lys Asp Met Glu Ser Leu Arg Gly Asn Gly			
209	220 225 230 235			
211	gaa gga gaa cgt aaa tca ttc gag cgg ata tat gat tat gat gtg tac	771		
212	Glu Gly Glu Arg Lys Ser Phe Glu Arg Ile Tyr Asp Tyr Asp Val Tyr			
213	240 245 250			
215	aac gat ctc gga gat ccg gat gga agc tta gat cta gca cgg ccg gtg	819		
216	Asn Asp Leu Gly Asp Pro Asp Gly Ser Leu Asp Leu Ala Arg Pro Val			
217	255 260 265			
219	ctc ggt ggc gag aca cat ccg tac cct agg ccg tgc cgt act ggt cgc	867		
220	Leu Gly Gly Glu Thr His Pro Tyr Pro Arg Arg Cys Arg Thr Gly Arg			
221	270 275 280			
223	aaa atg tcc tct aaa gat ccg tta aca gaa agc aga act acg ctc cct	915		
224	Lys Met Ser Ser Lys Asp Pro Leu Thr Glu Ser Arg Thr Thr Leu Pro			
225	285 290 295			
227	ttt tat gta cct gcg gat gaa gat ttt tca gag ata aag agt gtg aac	963		
228	Phe Tyr Val Pro Ala Asp Glu Asp Phe Ser Glu Ile Lys Ser Val Asn			
229	300 305 310 315			
231	ttt gga gca aaa act tta tac tct gtg ctt cat gga gtt gta cca atg	1011		
232	Phe Gly Ala Lys Thr Leu Tyr Ser Val Leu His Gly Val Val Pro Met			
233	320 325 330			
235	cta gac tca att gta aca gac aaa gac aag ggg ttt cca tta ttc aca	1059		
236	Leu Asp Ser Ile Val Thr Asp Lys Asp Lys Gly Phe Pro Leu Phe Thr			
237	335 340 345			
239	tcc ata gat ttg ctt tat aat gaa ggt gtt aat gtt cct tct cct gac	1107		
240	Ser Ile Asp Leu Leu Tyr Asn Glu Gly Val Asn Val Pro Ser Pro Asp			
241	350 355 360			
243	aat gga att cta agt gct tta cct aga ctt gtc aaa ggg gct act gat	1155		
244	Asn Gly Ile Leu Ser Ala Leu Pro Arg Leu Val Lys Gly Ala Thr Asp			
245	365 370 375			
247	gcc gca aat acc gtt atc aag ttc gag acc ccc gaa acc att gat aga	1203		
248	Ala Ala Asn Thr Val Ile Lys Phe Glu Thr Pro Glu Thr Ile Asp Arg			
249	380 385 390 395			

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251	gac gca ttc tca tgg ttc cgt gat gaa gag ttc tgc cgg caa atg ctt	1251
252	Asp Ala Phe Ser Trp Phe Arg Asp Glu Glu Phe Cys Arg Gln Met Leu	
253	400 405 410	
255	gcc ggt att aat cct tgt cgc ata caa ttg gtt acg gaa tgg cca ttg	1299
256	Ala Gly Ile Asn Pro Cys Arg Ile Gln Leu Val Thr Glu Trp Pro Leu	
257	415 420 425	
259	atg agt aaa ctg gac cct gaa atc tat gga cca gct gag tca gca att	1347
260	Met Ser Lys Leu Asp Pro Glu Ile Tyr Gly Pro Ala Glu Ser Ala Ile	
261	430 435 440	
263	aca aag gag att gta gag gaa gag att aaa ggt ttc atg act ctt gag	1395
264	Thr Lys Glu Ile Val Glu Glu Glu Ile Lys Gly Phe Met Thr Leu Glu	
265	445 450 455	
267	gag gct tta gca caa aag aag ctg ttt atg ctg gat tat cat gat ctg	1443
268	Glu Ala Leu Ala Gln Lys Lys Leu Phe Met Leu Asp Tyr His Asp Leu	
269	460 465 470 475	
271	ctc ttg cct tat gtt aac aaa acg gag gct gaa ggg aga act ttg tat	1491
272	Leu Leu Pro Tyr Val Asn Lys Thr Glu Ala Glu Gly Arg Thr Leu Tyr	
273	480 485 490	
275	ggt tca aga act tta atg ttc ctt act cct gct gga aca tta agg cca	1539
276	Gly Ser Arg Thr Leu Met Phe Leu Thr Pro Ala Gly Thr Leu Arg Pro	
277	495 500 505	
279	cta gcc att gag ctg act cgc cca cca gtt gat ggg aaa cca cag tgg	1587
280	Leu Ala Ile Glu Leu Thr Arg Pro Pro Val Asp Gly Lys Pro Gln Trp	
281	510 515 520	
283	aaa cat gtt tac aca ccc gct tgg gat gct aca ggt gca tgg ctt tgg	1635
284	Lys His Val Tyr Thr Pro Ala Trp Asp Ala Thr Gly Ala Trp Leu Trp	
285	525 530 535	
287	aag cta gcc aag gct cat gtc ctt gcc cat gat tct agc tat cac caa	1683
288	Lys Leu Ala Lys Ala His Val Leu Ala His Asp Ser Ser Tyr His Gln	
289	540 545 550 555	
291	ctt gtt agc cat tgg cta aga aca cat tgt gct acc gaa cct tac att	1731
292	Leu Val Ser His Trp Leu Arg Thr His Cys Ala Thr Glu Pro Tyr Ile	
293	560 565 570	
295	att gct acc aat cgc caa ctc agt caa atg cat cca att cga cga ttt	1779
296	Ile Ala Thr Asn Arg Gln Leu Ser Gln Met His Pro Ile Arg Arg Phe	
297	575 580 585	
299	cta ctc cct cat ttc cgt tac act atg caa att aat tct cta gct aga	1827
300	Leu Leu Pro His Phe Arg Tyr Thr Met Gln Ile Asn Ser Leu Ala Arg	
301	590 595 600	
303	ctt tta ctc gtc aat gcc atg ggt atc ata gag tca aca ttt tct cct	1875
304	Leu Leu Leu Val Asn Ala Met Gly Ile Ile Glu Ser Thr Phe Ser Pro	
305	605 610 615	
307	gga aga tat tgt atg caa att tcc tct gat gca tat gat cag caa tgg	1923
308	Gly Arg Tyr Cys Met Gln Ile Ser Ser Asp Ala Tyr Asp Gln Gln Trp	
309	620 625 630 635	
311	cgt ttt gat cat gaa gcg ctt ccg gcc gac cta att agc agg ggt atg	1971
312	Arg Phe Asp His Glu Ala Leu Pro Ala Asp Leu Ile Ser Arg Gly Met	
313	640 645 650	
315	gcg gtt gaa gat cca acc gca cca tat ggt gta aaa cta aca atc gag	2019

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L:150 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:3
L:520 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:5
L:524 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:5
L:528 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:5
L:558 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:6
L:731 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8
L:823 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:10
L:827 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:10
L:831 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:10